

## SEQUENCE SUBMISSION

SEQ ID NO: 1 is primate DCRS6 nucleotide sequence.  
 SEQ ID NO: 2 is primate DCRS6 polypeptide sequence.  
 SEQ ID NO: 3 is primate DCRS6 reverse translation.  
 SEQ ID NO: 4 is rodent DCRS6 nucleotide sequence.  
 SEQ ID NO: 5 is rodent DCRS6 polypeptide sequence.  
 SEQ ID NO: 6 is rodent DCRS6 reverse translation.  
 SEQ ID NO: 7 is primate DCRS7 nucleotide sequence.  
 SEQ ID NO: 8 is primate DCRS7 polypeptide sequence.  
 SEQ ID NO: 9 is primate DCRS7 reverse translation.  
 SEQ ID NO: 10 is rodent DCRS7 nucleotide sequence.  
 SEQ ID NO: 11 is rodent DCRS7 polypeptide sequence.  
 SEQ ID NO: 12 is rodent DCRS7 reverse translation.  
 SEQ ID NO: 13 is primate DCRS8 nucleotide sequence.  
 SEQ ID NO: 14 is primate DCRS8 polypeptide sequence.  
 SEQ ID NO: 15 is primate DCRS8 reverse translation.  
 SEQ ID NO: 16 is primate DCRS9 nucleotide sequence.  
 SEQ ID NO: 17 is primate DCRS9 polypeptide sequence.  
 SEQ ID NO: 18 is primate DCRS9 reverse translation.  
 SEQ ID NO: 19 is rodent DCRS9 nucleotide sequence.  
 SEQ ID NO: 20 is rodent DCRS9 polypeptide sequence.  
 SEQ ID NO: 21 is rodent DCRS9 reverse translation.  
 SEQ ID NO: 22 is primate DCRS10 nucleotide sequence.  
 SEQ ID NO: 23 is primate DCRS10 polypeptide sequence.  
 SEQ ID NO: 24 is primate DCRS10 reverse translation.  
 SEQ ID NO: 25 is rodent DCRS10 nucleotide sequence.  
 SEQ ID NO: 26 is rodent DCRS10 polypeptide sequence.  
 SEQ ID NO: 27 is rodent DCRS10 reverse translation.  
 SEQ ID NO: 28 is primate IL-17 receptor peptide sequence.  
 SEQ ID NO: 29 is rodent IL-17 receptor peptide sequence.  
 SEQ ID NO: 30 is worm IL-17 receptor peptide sequence.  
 SEQ ID NO: 31 is worm DCRS6 nucleotide sequence.

<110> Gorman, Daniel M.

<120> Mammalian Receptor Proteins; Related Reagents and Methods

<130> DX01170K US

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<150> US 60/206,862

<151> 2000-05-24

<160> 31

<170> PatentIn Ver. 2.0

<210> 1

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<213> Unknown

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<223> Description of Unknown Organism: primate; surmised  
Homo sapiens

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cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp	
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ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca	192
Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser	
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Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg	
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70 75 80	
tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag	336
Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln	
85 90 95	
acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct	384
Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro	
100 105 110	
gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat	432
Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
115 120 125	
gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat ttc acc tca	480
Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser	
130 135 140 145	
cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag tgt gtc aag	528
Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys	
150 155 160	
gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag aag aat gag	576
Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu	
165 170 175	
gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga aac aga tac	624
Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr	
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Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val	
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Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro	
230 235 240	
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Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys	
245 250 255	
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Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro	
260 265 270	
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Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp	
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Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys	
290 295 300 305	
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Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu	
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Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe	
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Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys	
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Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala	
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gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc	1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro	
390 395 400	
agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc	1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys	
405 410 415	
agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac	1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr	
420 425 430	

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ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc 1392  
 Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys  
 435 440 445

ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt 1440  
 Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu  
 450 455 460 465

ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc 1488  
 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys  
 470 475 480

cac gat ggc tgc tgc tcc ttg tagccacccc atgagaagca agagacctta 1539  
 His Asp Gly Cys Cys Ser Leu  
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aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgacccctga agcttactat 1599

gcagcctaca aacagcctta gtaattaaaa cattttatata caataaaatt ttcaaattat 1659

gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt 1719

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Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 35 40 45 50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 55 60 65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 70 75 80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr  
 85 90 95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val  
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Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala  
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Glu	Asn	Ser	Gln	Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	
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Arg	Glu	Ile	Asp	Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	
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Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu  
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 gaytaywsna thytnatgaa ygtnwsntgg gtntymngng cngaygcnws nathmgnytn 240  
 ytnaargcna cnaarathtg ygtnacnggn aarwsnaayt tycarwsnta ywsntgygtn 300  
 mgntgyaayt ayacngargc nttycaracn caracnmgnc cnwsnggngg naartggacn 360  
 ttywsntaya thggnttycc ngtngarytn aayacngtnt ayttyathgg ngcncaayaay 420  
 athccnaayg cnaayatgaa ygargayggn ccnwsnatgw sngtnaaytt yacnwsnccn 480  
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 gayaayaaya arwsnaarcc nggnggntgg ytnccnytny tnytnytnws nytntngtn 900  
 gcnacntggg tnytnngtgc nggnathtay ytnatgtggm gncaygarmg nathaaraar 960  
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 cayaartayg tngtngtnta yttymngnar athgayacna argaygayta yaaygcnytn 1380  
 wsngtntgye cnaartayca yytnatgaar gaygcnaacng cnttytgygc ngarytnytn 1440  
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 ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc 96  
 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro  
 20 25 30  
 caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc 144  
 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu  
 35 40 45  
 aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat 192  
 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His  
 50 55 60  
 gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa 240  
 Asp Ser Cys Ser Pro Leu  
 65 70

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 agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac 480  
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 gggtgggtct gtcttgcaat gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt 600

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 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu  
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 acngcnttyc ayacngaryt nytnaargcn acncarwsna tgwsngtnaa raarmgnwsn 180  
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atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
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tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc 324
Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25

ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg 372
Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40

cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt 420
His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60

gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg 468
Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75

gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg 516
Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90

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Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105

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Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Glu Glu Val Gln Val
110 115 120

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Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140

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Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
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 Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala  
 175 180 185  
 ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt 852  
 Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val  
 190 195 200  
 ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat 900  
 Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn  
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 Gln Val Gln Gly Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly  
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 ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt 996  
 Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys  
 240 245 250  
 att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc 1044  
 Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys  
 255 260 265  
 ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc 1092  
 Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala  
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 Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys  
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 Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp  
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Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
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Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys	Ile	Gln	Val	Trp				
			240					245					250						
Ser	Leu	Glu	Pro	Asp	Ser	Glu	Arg	Val	Glu	Phe	Cys	Pro	Phe	Arg	Glu				
		255					260					265							
Asp	Pro	Gly	Ala	His	Arg	Asn	Leu	Trp	His	Ile	Ala	Arg	Leu	Arg	Val				
		270				275					280								
Leu	Ser	Pro	Gly	Val	Trp	Gln	Leu	Asp	Ala	Pro	Cys	Cys	Leu	Pro	Gly				
285					290				295						300				
Lys	Val	Thr	Leu	Cys	Trp	Gln	Ala	Pro	Asp	Gln	Ser	Pro	Cys	Gln	Pro				
				305					310					315					
Leu	Val	Pro	Pro	Val	Pro	Gln	Lys	Asn	Ala	Thr	Val	Asn	Glu	Pro	Gln				
			320					325					330						
Asp	Phe	Gln	Leu	Val	Ala	Gly	His	Pro	Asn	Leu	Cys	Val	Gln	Val	Ser				
		335					340					345							
Thr	Trp	Glu	Lys	Val	Gln	Leu	Gln	Ala	Cys	Leu	Trp	Ala	Asp	Ser	Leu				
		350				355					360								
Gly	Pro	Phe	Lys	Asp	Asp	Met	Leu	Leu	Val	Glu	Met	Lys	Thr	Gly	Leu				
365					370					375					380				
Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys	Thr	Pro	Leu				
				385					390					395					
Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu	Glu	Leu	Leu				
			400					405					410						
Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	Asn	Asp	Asp	Asn				
		415					420					425							
Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	Arg	Arg				
		430				435					440								
Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe				
445					450					455					460				
Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser				
				465				470						475					
Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	Gly	Tyr	Glu	Arg				

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490

Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu  
670 675

<213> reverse translation

<223> n may be a, c, g, or t

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ytntgggayg	gngaygtnyt	ntgyytnccn	ggnwsnytn	c arwsngcncc	nggnccngtn	180
ytngtnccna	cnmgnytnca	racngarytn	gtnytnmgnt	gyccncaraa	racngaytgy	240
gcnytnctgy	tnmgngtngt	ngtncaaytn	gcngtncaay	gncaytgggc	ngarccngar	300

gargcnggna arwsngayws ngarytnicar garwsnmgna aygcnwsnyt ncargcncar 360  
 gtngtnytnw snttycargc ntayccnath gcnmgntgyg cnytnytnga rgtncargtn 420  
 ccngcngayy tngtncarcc nggncarwsn gtnggnwsng cngtnttyga ytgyttygar 480  
 gcnwsnytnng gngcngargt ncarathtgg wsntayacna arccnmgnta ycaraargar 540  
 ytnaayytna encarcaryt nccngaytgy mgnggnytnng argtnmgnga ywsnathcar 600  
 wsntgytggg tnytnccntg gytnaaygt nwsnacngayg gngayaaygt nytnytnacn 660  
 ytngaygt nwsngargarca rgayttywsn tyytnytnnt ayytnmgnc ngtncngay 720  
 gcnytnaarw snytntggt yaaraayytn acnggncnc araayathac nytnaaycay 780  
 acngayytn tncntgyt ntgyathcar gtntggwsny tngarccnga ywsngarmgn 840  
 gtngarttyt gycnttymg ngargayccn ggngcncaym gnaayytn gcyathgcn 900  
 mgnytnmgng tnytnwsncc ngngntntgg carytngayg cncntgytg yytnccnggn 960  
 aargtnacny tntgytggca rgcncngay carwsnccnt gycarccnyt ngtnccncn 1020  
 gtncncara araaygcnc ngtnaaygar ccncargayt tycarytngt ngcnggncay 1080  
 ccnaayytn gygtncargt nwsnacntgg garaargtnc arytncargc ntgyytntg 1140  
 gcngaywsny tnggncntt yaargaygay atgytnytn tngaratgaa racnggnytn 1200  
 aayaayacnw sngtntgygc nytngarccn wsnggntgya cncnytncc nwsnatggcn 1260  
 wsnacnmng cngcnmgnyt ngngngargar ytnytncarg ayttymgnws ncaycartgy 1320  
 atgcarytn ggaaygayga yaayatgggn wsnytntggt cntgyccnat ggayaartay 1380  
 athcaymgnm gntgggtnyt ngtntggytn gcntgyytn tnytngcngc ngcnytnntty 1440  
 tyyttnytn tnytnaaraa rgaymgnmgn aargcngcnm gnggnwsnmg nacngcnytn 1500  
 ytnytnacayw sngcngaygg ngcnggntay garmgnytn tnggngcnyt ngcnwsngcn 1560  
 ytnwsncara tgccnytnmg ngtngcngtn gayytntgw snmgngnga rytwnsngcn 1620  
 cayggngcny tngcntggt ycaycaycar mgnmgngna thytncarga rggngngtn 1680  
 gtnathytn tnttywsncc ngcngcngtn gncartgyc arcartggyt ncarytnicar 1740  
 acngtngar cnggncnc yaaygcnytn gcngcntggy tnwsntgygt nytnccngay 1800  
 tyytncarg gnmngcnac nggngntay gtngngntnt aytygaygg nytnytnacay 1860  
 ccngaywsng tncnwsncc nttymngtn gncnytnnt tywsnytncc nwsncarytn 1920  
 ccngcntty tngaygcnyt ncarggnggn tgywsnacw sngcngngm nccngcngay 1980  
 mgngtnarm gngtnacna rcnytnmgn wsnngcnytn aywsntgyac nwsnwsnwsn 2040  
 gargcncng gntgytgyga rgartgggay ytnngncnt gyacnacnyt ngar 2094

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<210> 13  
 <211> 2786  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>  
 <221> CDS  
 <222> (70)..(2283)

<220>  
 <221> mat\_peptide  
 <222> (118)..(2283)

<220>  
 <221> misc\_feature  
 <222> (9)..(134)  
 <223> Xaa translation (9, 18,26, 109,120, 134) depends  
 on genetic code

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 cgcacggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111  
 Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val  
 -15 -10 -5  
 aac gcc tgc ctc aac ggc tgc cag ctg gct gtn gcc gct ggc ggg tcc 159  
 Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser  
 -1 1 5 10  
 ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca 207  
 Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro  
 15 20 25 30  
 gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat 255  
 Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn  
 35 40 45  
 tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc 303  
 Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala  
 50 55 60  
 cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc 351  
 Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val  
 65 70 75  
 acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga 399  
 Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly  
 80 85 90  
 ttt cgg gta ata ctg gag gag ctg aag tgc gag gga aga cag ngc caa 447  
 Phe Arg Val Ile Leu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln  
 95 100 105 110  
 caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga 495

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Gln	Leu	Ile	Leu	Lys	Asp	Pro	Lys	Gln	Xaa	Asn	Ser	Ser	Phe	Lys	Arg		
				115					120					125			
act	gga	atg	gaa	tct	caa	cct	ttt	ctg	aat	atg	aaa	ttt	gaa	acg	gat	543	
Thr	Gly	Met	Glu	Ser	Gln	Pro	Xaa	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp		
			130					135					140				
tat	ttc	gta	agg	ttg	tcc	ttt	tcc	ttc	att	aaa	aac	gaa	agc	aat	tac	591	
Tyr	Phe	Val	Arg	Leu	Ser	Phe	Ser	Phe	Ile	Lys	Asn	Glu	Ser	Asn	Tyr		
		145					150					155					
cac	cct	ttc	ttc	ttt	aga	acc	cga	gcc	tgt	gac	ctg	ttg	tta	cag	ccg	639	
His	Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro		
	160					165					170						
gac	aat	cta	gct	tgt	aaa	ccc	ttc	tgg	aag	cct	cgg	aac	ctg	aac	atc	687	
Asp	Asn	Leu	Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile		
175					180					185					190		
agc	cag	cat	ggc	tcg	gac	atg	cag	gtg	tcc	ttc	gac	cac	gca	ccg	cac	735	
Ser	Gln	His	Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His		
			195					200					205				
aac	ttc	ggc	ttc	cgt	ttc	ttc	tat	ctt	cac	tac	aag	ctc	aag	cac	gaa	783	
Asn	Phe	Gly	Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu		
			210					215					220				
gga	cct	ttc	aag	cga	aag	acc	tgt	aag	cag	gag	caa	act	aca	gag	atg	831	
Gly	Pro	Phe	Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met		
		225					230					235					
acc	agc	tgc	ctc	ctt	caa	aat	gtt	tct	cca	ggg	gat	tat	ata	att	gag	879	
Thr	Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu		
	240					245					250						
ctg	gtg	gat	gac	act	aac	aca	aca	aga	aaa	gtg	atg	cat	tat	gcc	tta	927	
Leu	Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu		
255					260					265					270		
aag	cca	gtg	cac	tcc	ccg	tgg	gcc	ggg	ccc	atc	aga	gcc	gtg	gcc	atc	975	
Lys	Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile		
				275				280					285				
aca	gtg	cca	ctg	gta	gtc	ata	tcg	gca	ttc	gcg	acg	ctc	ttc	act	gtg	1023	
Thr	Val	Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val		
			290					295					300				
atg	tgc	cgc	aag	aag	caa	caa	gaa	aat	ata	tat	tca	cat	tta	gat	gaa	1071	
Met	Cys	Arg	Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu		
		305					310					315					
gag	agc	tct	gag	tct	tcc	aca	tac	act	gca	gca	ctc	cca	aga	gag	agg	1119	
Glu	Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg		
		320				325					330						
ctc	cgg	ccg	cgg	ccg	aag	gtc	ttt	ctc	tgc	tat	tcc	agt	aaa	gat	ggc	1167	
Leu	Arg	Pro	Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly		
335					340				345					350			
cag	aat	cac	atg	aat	gtc	gtc	cag	tgt	ttc	gcc	tac	ttc	ctc	cag	gac	1215	

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Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp  
 355 360 365  
 ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc 1263  
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu  
 370 375 380  
 tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc 1311  
 Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser  
 385 390 395  
 cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac 1359  
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp  
 400 405 410  
 aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga 1407  
 Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly  
 415 420 425 430  
 gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag 1455  
 Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln  
 435 440 445  
 gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac 1503  
 Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr  
 450 455 460  
 ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt 1551  
 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser  
 465 470 475  
 acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg 1599  
 Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu  
 480 485 490  
 cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag 1647  
 His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln  
 495 500 505 510  
 ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac 1695  
 Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr  
 515 520 525  
 gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg 1743  
 Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp  
 530 535 540  
 ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg 1791  
 Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg  
 545 550 555  
 gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt tta aat gat gtc 1839  
 Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val  
 560 565 570  
 atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg 1887  
 Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala  
 575 580 585 590  
 gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag 1935

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Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln  
595 600 605

cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt 1983  
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly  
610 615 620

agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa gcc ggc agc ccc 2031  
Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro  
625 630 635

tcg gac atg ccg cgg gac tca ggc atc tat gac tcg tct gtg ccc tca 2079  
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser  
640 645 650

tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg acg gac cag aca 2127  
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr  
655 660 665 670

gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct tca ggc ctg ggt 2175  
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly  
675 680 685

gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc tct tct ggg tca 2223  
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser  
690 695 700

tgc aaa gca gat ctt ggt tgc cgc agc tac act gat gaa ctc cac gcg 2271  
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala  
705 710 715

gtc gcc cct ttg taacaaaacg aaagagtcta agcattgccca ctttagctgc 2323  
Val Ala Pro Leu  
720

tgccctccctc tgattcccca gctcatctcc ctggttgcat ggcccacttg gagctgaggt 2383

ctcatacaag gatatttgga gtgaaatgct ggccagtact tgttctccct tgccccaacc 2443

ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg 2503

catgtccata aggtctgaca acagcttgcc aaatttggtt agtccttgga tcagagcctg 2563

ttgtgggagg tagggaggaa atatgtaaag aaaaacagga agatacctgc actaatcatt 2623

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683

gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743

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<211> 738  
<212> PRT  
<213> Unknown

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-15 -10 -5 -1

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Cys Leu Asn Gly Ser Gln Leu Ala Xaa Ala Ala Gly Gly Ser Gly Arg  
 1 5 10 15  
 Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro Ala Ser  
 20 25 30  
 Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr  
 35 40 45  
 Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn  
 50 55 60  
 Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile  
 65 70 75 80  
 Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg  
 85 90 95  
 Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln Gln Leu  
 100 105 110  
 Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg Thr Gly  
 115 120 125  
 Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe  
 130 135 140  
 Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr His Pro  
 145 150 155 160  
 Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn  
 165 170 175  
 Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln  
 180 185 190  
 His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe  
 195 200 205  
 Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro  
 210 215 220  
 Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser  
 225 230 235 240  
 Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val  
 245 250 255  
 Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro  
 260 265 270  
 Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val  
 275 280 285  
 Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys  
 290 295 300  
 Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser  
 305 310 315 320

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Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg  
 325 330 335  
 Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn  
 340 345 350  
 His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys  
 355 360 365  
 Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg  
 370 375 380  
 Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe  
 385 390 395 400  
 Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys  
 405 410 415  
 Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu  
 420 425 430  
 Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys  
 435 440 445  
 Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp  
 450 455 460  
 Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys  
 465 470 475 480  
 Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser  
 485 490 495  
 Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser  
 500 505 510  
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala  
 515 520 525  
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu  
 530 535 540  
 Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro  
 545 550 555 560  
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys  
 565 570 575  
 Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val  
 580 585 590  
 Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly  
 595 600 605  
 Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala  
 610 615 620  
 Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp  
 625 630 635 640

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Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu  
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr  
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu  
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys  
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala  
705 710 715 720

Pro Leu

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<211> 2214  
<212> DNA  
<213> reverse translation

<220>  
<221> misc\_feature  
<222> (1)..(2214)  
<223> n may be a, c, g, or t

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tggnnnggng tnggncngc nwsnmgnaay wsnggnytn tnaayathac nttyaartay 180  
gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnathgcnga ygcncaraay 240  
athacnathw sncartaygc ntgycaygay cargtngcng tnacnathyt ntggwsnccn 300  
ggngcnytn gnatgartt yytnaarggn ttymngntna thytnngarga rytnaarwsn 360  
garggmngc arnnncarca rytnathytn aargayccna arcarnnnaa ywsnwsntty 420  
aarmgnacng gnatggarws ncarccnnnn ytnaayatga arttygarac ngaytaytty 480  
gtnmngnytnw snttywsntt yathaaraay garwsnaayt aycayccntt yttyttymgn 540  
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ccnmgnaay tnaayathws ncarcayggn wsngayatgc argtnwsntt ygaycaygc 660  
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ttyaarmgna aracntgyaa rcargarcar acnacngara tgacnwsntg yytnytnear 780  
aaygtnwsnc cnggngayta yathathgar ytngtngayg ayacnaayac nacnmgnaar 840  
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 aarcarttyg tncnttyca yccnccnccn ytnmgntaym gngarccngt nytnagaraar 1740  
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 wsncarcayg gnggnytna ycargayggg gargcnmgnc cngcnytna yggnwsngcn 1920  
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 <212> DNA  
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gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc	96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
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cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
30 35 40	
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Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
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Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
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aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
140 145 150	
agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	
155 160 165	
ctg cct gag gcc cgg gct att cgg gtg acc ata tot tca ggc cct gag	624
Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu	
170 175 180 185	
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Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Leu	
190 195 200	

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Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val	
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gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc	768
Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser	
220 225 230	
tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc	816
Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser	
235 240 245	
tgg cca gaa gcc tat ggc tgc gac ttc tgg aag tca gtg cac ttc act	864
Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr	
250 255 260 265	
gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc	912
Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys	
270 275 280	
cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc	960
Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr	
285 290 295	
ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg	1008
Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp	
300 305 310	
tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta	1056
Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val	
315 320 325	
caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac	1104
Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His	
330 335 340 345	
cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc	1152
Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala	
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cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt	1200
Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser	
365 370 375	
gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc	1248
Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro	
380 385 390	
gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg	1296
Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp	
395 400 405	
aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg	1344
Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu	
410 415 420 425	
atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc	1392
Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala	
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 His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro  
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 Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly  
                       30                      35                      40  
 Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys  
                       45                      50                      55  
 Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg  
           60                      65                      70  
 Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys  
       75                      80                      85  
 Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg  
   90                      95                     100                     105  
 Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp  
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 Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val  
                      125                     130                     135  
 Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn  
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 Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu  
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 Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu  
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 Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val  
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 Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser  
   235                     240                     245  
 Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr  
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 Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys  
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 Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr  
      285                     290                     295  
 Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp  
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Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val  
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 Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His  
 330 335 340 345  
 Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala  
 350 355 360  
 Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser  
 365 370 375  
 Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro  
 380 385 390  
 Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp  
 395 400 405  
 Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu  
 410 415 420 425  
 Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala  
 430 435 440  
 Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val  
 445 450 455  
 Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly  
 460 465 470  
 Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val  
 475 480 485  
 Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu  
 490 495 500 505  
 Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr  
 510 515 520  
 Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro  
 525 530 535  
 Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg  
 540 545 550  
 Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp  
 555 560 565  
 Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp  
 570 575 580 585  
 Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala  
 590 595 600  
 Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu  
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 <211> 1971  
 <212> DNA  
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<220>  
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 gcnwsncaya cngargtnyt nccnathwsn ytngcngcnc cnggnggncc nwsnwsnccn 180  
 carwsnytn gngtntgyga rwsnggnacn gtncngcng tntgygcnws nathtgytgy 240  
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 tgyytngtng tnacntgyt nmgnmgngcn athacnttyc cnwsnccncc ncaracnwsn 420  
 ccnacmgng aytygcnyt naarggnccn ayytnmgna thcarmgna yggnaargtn 480  
 ttyccngayt ggacncayaa rggnatggar gtnggnacng gntayaaymg nmgntgggt 540  
 carytnwsng gnggnccnga rtywsntty gayytnytn cngargcnmg ngcnathmgn 600  
 gtnacnathw snwsnggncc ngargtnwsn gtnmgnytnt gycaycartg ggcnytngr 660  
 tgygargary tnwsnwsncc ntaygaygt ncarathg tnwsnggngg ncayacngtn 720  
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 gayacngtnm gnmgnaaraa rtgyccntty carwsntggc cngargcnta yggnwsngay 840  
 ttytggaarw sngtnaytt yacngaytay wsnarcaya cncaratggt natggcnyn 900  
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 ytntgyaarg ayytnccnaa ygcnacngcn mgngarwsng ayggntggta ygtnytngr 1020  
 aargtngayy tncayccna rytntgytty aargtnarc cntggtyws nttyggnaay 1080  
 wsnwsncayg tngartgycc ncaycaracn ggnwsnytna cnwsntggaa ygtwnsnatg 1140  
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 wsnargtn ggmgnwsnga ygtncartty gcntggaarc ayytnytn gcnaygtn 1320

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wsntaymgnc ayytnggny nytnathytn gcnynytng cnynyttnac nytnytnggn 1380  
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 ccnmngntaym gnytnytng ngayytncn mgnytntnm gngcnytna ygcnmgnccn 1860  
 ttygcngarg cnacnwsntg gggngmnytn ggngcnmgnc armngmgnca rwsnmgnytn 1920  
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 Mus musculus

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 Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu  
 -20 -15  
 tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158  
 Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala  
 -10 -5 -1 1  
 tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206  
 Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg  
 5 10 15 20  
 gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254  
 Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu  
 25 30 35  
 gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302

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 Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu  
                     55                    60                    65

tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac 398  
 Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His  
                     70                    75                    80

aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga 446  
 Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg  
                     85                    90                    95                    100

gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc 494  
 Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe  
                     105                    110                    115

tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct 542  
 Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro  
                     120                    125                    130

gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa 590  
 Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu  
                     135                    140                    145

tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga 638  
 Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly  
                     150                    155                    160

ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc 686  
 Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys  
                     165                    170                    175                    180

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 Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val  
                     185                    190                    195

cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa 782  
 Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln  
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Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe  
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 Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys  
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 Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser  
 45 50 55  
 Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His  
 60 65 70  
 Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr  
 75 80 85  
 Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu  
 90 95 100 105  
 Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu  
 110 115 120  
 Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala  
 125 130 135  
 Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser  
 140 145 150  
 Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp  
 155 160 165  
 Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr  
 170 175 180 185  
 Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly  
 190 195 200  
 Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr  
 205 210 215  
 Thr Ala Ser  
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 gcntaymgng tngayaarmg nttygcnggn ytncartggg gntgggttycc nytnytnngtn 180

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mgnaarwsna arwsnccncc naarttygar gaytaytggm gncaymgnac nccngcnwsn 240  
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 ccnwsnwsng cnathwsnca ymgnggncar mgnacnaarm gngcncarcc nwsngcngcn 360  
 garggnmgng arcayytncc ngargcnggn wsncaraart gyggnggncc ngarttywsn 420  
 ttygayytny tncngargt ncargcngtn mgngtnacna thcngcngg nccnaargcn 480  
 mgngtnmgny tntgytayca rtgggcnyn tn gartgygarg ayytnwsnws nccnttygay 540  
 acncaraara thgtnwsngg nggncayacn gtngayytncc cntaygartt yytnytnccn 600  
 tgyatgtgya thgargcnws ntayytnear gargayacng tnmgnmgnaa rwsngtnccn 660  
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 acngcnwsn 729

<210> 22  
 <211> 2377  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>  
 <221> CDS  
 <222> (180)..(1874)

<400> 22  
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 gagagccgac taccctccgg gccagtcctg tctgtccgtg gtggatctaa gaaactaga 179  
 atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227  
 Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro  
 1 5 10 15  
 agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275  
 Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser  
 20 25 30  
 gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323  
 Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser  
 35 40 45  
 gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371  
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His  
 50 55 60  
 tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc 419  
 Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val  
 65 70 75 80

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acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc 467  
 Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys  
 85 90 95

agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca 515  
 Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala  
 100 105 110

gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag 563  
 Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu  
 115 120 125

cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag 611  
 His Gln Phe Ser Phe Met Gln Lys Arg Asn Gln Trp Leu Val Ser Gln  
 130 135 140

ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac 659  
 Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp  
 145 150 155 160

caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag 707  
 Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu  
 165 170 175

atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg 755  
 Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu  
 180 185 190

cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc 803  
 Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly  
 195 200 205

atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc 851  
 Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro  
 210 215 220

cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa 899  
 Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu  
 225 230 235 240

cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc 947  
 Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser  
 245 250 255

cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat 995  
 Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp  
 260 265 270

cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa 1043  
 His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln  
 275 280 285

gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg 1091  
 Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val  
 290 295 300

aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc 1139  
 Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro  
 305 310 315 320

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tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
325 330 335	
ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
340 345 350	
ggg gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
355 360 365	
gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
370 375 380	
cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
385 390 395 400	
cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg	1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
405 410 415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
420 425 430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag	1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu	
435 440 445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc	1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro	
450 455 460	
aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat	1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp	
465 470 475 480	
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag	1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu	
485 490 495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc	1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe	
500 505 510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat	1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His	
515 520 525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg	1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu	
530 535 540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt	1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu	
545 550 555 560	

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cag gtg gtt ccc ttg tgacaccggt catccccaga tcaactgaggc caggccatgt 1914  
 Gln Val Val Pro Leu  
 565

ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctgggt 1974  
 tttttctgtt cctccccgag aggcctctg gccccagga aacctgttgt gcagagctct 2034  
 tccccggaga cctccacaca cctgggttt gaagtggagt ctgtgactgc tctgcattct 2094  
 ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga 2154  
 tgtgtccatt ctgggcctct cagtgttag caagtagata atgtaaggga tgtggcagca 2214  
 aatggaaatg actacaaaca ctctcctatc aatcatttca ggctactttt atgagtttagc 2274  
 cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc 2334  
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<210> 23  
 <211> 565  
 <212> PRT  
 <213> Unknown

<400> 23

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Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser  
 20 25 30

Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser  
 35 40 45

Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His  
 50 55 60

Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val  
 65 70 75 80

Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys  
 85 90 95

Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala  
 100 105 110

Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu  
 115 120 125

His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln  
 130 135 140

Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp  
 145 150 155 160

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu  
 165 170 175

09363318 "0512301

Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu  
 180 185 190  
 Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly  
 195 200 205  
 Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro  
 210 215 220  
 Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu  
 225 230 235 240  
 Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser  
 245 250 255  
 Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp  
 260 265 270  
 His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln  
 275 280 285  
 Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val  
 290 295 300  
 Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro  
 305 310 315 320  
 Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly  
 325 330 335  
 Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala  
 340 345 350  
 Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln  
 355 360 365  
 Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn  
 370 375 380  
 Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu  
 385 390 395 400  
 Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val  
 405 410 415  
 Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp  
 420 425 430  
 Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu  
 435 440 445  
 Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro  
 450 455 460  
 Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp  
 465 470 475 480  
 Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu  
 485 490 495

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Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe  
500 505 510

Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His  
515 520 525

Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu  
530 535 540

Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu  
545 550 555 560

Gln Val Val Pro Leu  
565

<210> 24

<211> 1695

<212> DNA

<213> reverse translation

<220>

<221> misc\_feature

<222> (1)..(1695)

<223> n may be a, c, g, or t

<400> 24

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aarcenathc cngartayws nccngargar garwsngarc cncngcncc naayathmgn 120  
aayatggcnc cnaaywsnyt nwsngcnccn acnatgytnc ayaaywsnws nggngaytty 180  
wsncargcnc aywsnacnyt naarytngcn aaycaycarm gncngtnws nmgnrcargtn 240  
acntgyytnm gnacncargt nytngargay wsngargayw snttytgymg nmgnrcayccn 300  
ggnytnngna argcnttycc nwsnggntgy wsngcngtnw sngarccngc nwsngarwsn 360  
gtngtnngng cnytnccngc ngarcaycar ttywsnttya tggaraarmg naaycartgg 420  
ytngtnwsnc arytnwsngc ngcnwsnccn gayacnggc aygaywsnga yaarwsngay 480  
carwsnytn cnaaygcnws ngcngaywsn ytnngnggnw sncargarat ggtncarmgn 540  
ccncarcnc aymgnaaymg ngcnggnytn gayytnccna cnathgayac nggntaygay 600  
wsncarcnc argaygtnyt nggnathmgn carytngarm gncnytncc nytnacnwsn 660  
gtntgytayc cncargayyt nccnmgnccn ytnmgnwsnm gngarttycc ncarttygar 720  
ccncarmgnt aycngcntg ygcncaratg ytnccncna ayytnwsncc ncaygcncn 780  
tggaaytayc aytaycaytg yccnggnwsn ccngaycayc argtnccnta yggncaygay 840  
tayccnmng cngcntayca rcargtnath carccngcny tncnggnca rccnytnccn 900  
ggngcnwsng tnmnggnytn ncayccngtn caraargtna thytnaayta yccnwsnccn 960

09663818 052301

tgggaycarg argarmgncc ngcncarmgn gaytgywsnt tyccnggnyt nccnmgncaay 1020  
 cargaycarc cncaycayca rccnccnaay mgngcnggng cncnggnga rwsnytngr 1080  
 tgyccngcng arytnmgncc ncargtnccn carcncncnw snccngcngc ngtnccnmgn 1140  
 ccncnwsna ayccncngc nmngngnacn ytnaaracnw snaayytnc nargarytn 1200  
 mgnaargtnt tyathacnta ywsnatggay acngcnatgg argtngtnaa rttygtnaay 1260  
 ttyytnytng tnaayggntt ycaracngcn athgayatht tygargaymg nathmgnggn 1320  
 athgayatha thaartggat ggarmgntay ytnmgngaya aracngtnat gathathgtn 1380  
 gcnathwsnc cnaartayaa rcargaygtn garggngcng arwsncaryt ngaygargay 1440  
 garcayggny tncayacnaa rtayathcay mgnatgatgc arathgartt yathaarc 1500  
 ggnwsnatga ayttymgntt yathccngtn ytnttyccna aygcnaaraa rgarcaygtn 1560  
 ccnactggy tncaraayac ncaygntay wsntggccna araayaaraa raayathytn 1620  
 ytnmgnytny tnmnggarga rgartaygtn gcnccncnm gnggncnyt nccnacnytn 1680  
 cargtngtnc cnytn 1695

<210> 25  
 <211> 1323  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:rodent; surmised  
 Mus musculus

<220>  
 <221> CDS  
 <222> (1) .. (1026)

<400> 25  
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 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe  
 1 5 10 15  
 gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96  
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro  
 20 25 30  
 tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144  
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro  
 35 40 45  
 tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192  
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala  
 50 55 60  
 tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240  
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly  
 65 70 75 80

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gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

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ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008  
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr  
                   325                                  330                                  335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc 1056  
 Leu Gln Val Val Pro Leu  
                   340

ctgttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcctgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt 1323

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 <211> 342  
 <212> PRT  
 <213> Unknown

<400> 26  
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Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro  
                   20                                  25                                  30

Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro  
                   35                                  40                                  45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala  
   50                                  55                                  60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly  
   65                                  70                                  75                                  80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp  
                   85                                  90                                  95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser  
                   100                                  105                                  110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly  
                   115                                  120                                  125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro  
   130                                  135                                  140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser  
   145                                  150                                  155                                  160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu  
                   165                                  170                                  175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val

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<210> 27
<211> 1026
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(1026)
<223> n amy be a, c, g, or t

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tayccnatga aygcncaryt nytnccncn cayccnwsnc ncargcncc ntggaaytgy 120
cartaytayt gyccnggngg nccntaycay caycargtnc ncayggnc a yggntayccn 180
ccngcngcng cntaycarca rgtnytn car ccngcnytn cnggncargt nytnccnggn 240
gcnmgngcnm gnggnccnmg nccngtn car aargtnathy tnaaygayws nwsnccncar 300
gaycargarg armgnccngc ncarmgngay ttywsnttyc cnmgnytncc nmngngaycar 360
ytntaymgnc cncnwsnaa yggngtngar gcncngarg arwsnytn ga yytnccngcn 420
garytnmgnc ncayggnc ncargcnccn wsnytn gng cngtnccnmg nccncnwsn 480

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<210> 28
<211> 207
<212> PRT
<213> Unknown
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<400> 28
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Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly Thr Glu
          20           25           30
Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala Gly Val
          35           40           45
Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
 50           55           60
Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala
 65           70           75           80
Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys
          85           90           95
Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp
          100          105          110
Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser
          115          120          125
Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro
          130          135          140
Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
145           150           155           160

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Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly Glu Leu  
165 170 175

Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu Arg Ala  
180 185 190

Ala Leu Asp Arg Phe Arg Asp Trp Gln Val Arg Cys Pro Asp Trp  
195 200 205

<210> 29

<211> 208

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: rodent; surmised  
Mus musculus

<400> 29

Arg Lys Val Trp Ile Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu  
1 5 10 15

Val Val Leu Lys Phe Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu  
20 25 30

Val Ala Leu Asp Leu Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val  
35 40 45

Met Thr Trp Val Ser Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser  
50 55 60

Lys Ile Ile Ile Leu Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala  
65 70 75 80

Ile Leu Gly Trp Ala Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp  
85 90 95

Lys Pro Ala Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro  
100 105 110

Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe  
115 120 125

Ser Gly Ile Cys Ser Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr  
130 135 140

Ser Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile  
145 150 155 160

Gln Asp Leu Glu Met Phe Glu Pro Gly Arg Met His His Val Arg Glu  
165 170 175

Leu Thr Gly Asp Asn Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys  
180 185 190

Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp  
195 200 205

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<210> 30  
 <211> 190  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism:worm; surmised  
 Caenorabditis elegans

<400> 30

Val	Lys	Val	Met	Ile	Val	Tyr	Ala	Asp	Asp	Asn	Asp	Leu	His	Thr	Asp
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Cys	Val	Lys	Lys	Leu	Val	Glu	Asn	Leu	Arg	Asn	Cys	Ala	Ser	Cys	Asp
			20					25					30		
Pro	Val	Phe	Asp	Leu	Glu	Lys	Leu	Ile	Thr	Ala	Glu	Ile	Val	Pro	Ser
		35					40					45			
Arg	Trp	Leu	Val	Asp	Gln	Ile	Ser	Ser	Leu	Lys	Lys	Phe	Ile	Ile	Val
	50					55					60				
Val	Ser	Asp	Cys	Ala	Glu	Lys	Ile	Leu	Asp	Thr	Glu	Ala	Ser	Glu	Thr
	65				70					75				80	
His	Gln	Leu	Val	Gln	Ala	Arg	Pro	Phe	Ala	Asp	Leu	Phe	Gly	Pro	Ala
				85					90					95	
Met	Glu	Met	Ile	Ile	Arg	Asp	Ala	Thr	His	Asn	Phe	Pro	Glu	Ala	Arg
			100					105					110		
Lys	Lys	Tyr	Ala	Val	Val	Arg	Phe	Asn	Tyr	Ser	Pro	His	Val	Pro	Pro
		115					120					125			
Asn	Leu	Ala	Ile	Leu	Asn	Leu	Pro	Thr	Phe	Ile	Pro	Glu	Gln	Phe	Ala
	130					135					140				
Gln	Leu	Thr	Ala	Phe	Leu	His	Asn	Val	Glu	His	Thr	Glu	Arg	Ala	Asn
	145				150					155					160
Val	Thr	Gln	Asn	Ile	Ser	Glu	Ala	Gln	Ile	His	Glu	Trp	Asn	Leu	Cys
				165					170					175	
Ala	Ser	Arg	Met	Met	Ser	Phe	Phe	Val	Arg	Asn	Pro	Asn	Trp		
			180					185					190		

<210> 31  
 <211> 178  
 <212> PRT  
 <213> Unknown

<220>

<223> Description of Unknown Organism:worm; surmised  
 Caenorabditis elegans

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&lt;400&gt; 31

Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp  
 1 5 10 15

Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val  
 20 25 30

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met  
 35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val  
 50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile  
 65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu  
 85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu  
 100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala  
 115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu  
 130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn  
 145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser  
 165 170 175

Asn Ser

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